

Shilin Tian

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

3,093
citations

257450

24
h-index

276875

41
g-index

47
all docs

47
docs citations

47
times ranked

4109
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative 3D genome architecture in vertebrates. <i>BMC Biology</i> , 2022, 20, 99.	3.8	25
2	Genomic selection and genetic architecture of agronomic traits during modern rapeseed breeding. <i>Nature Genetics</i> , 2022, 54, 694-704.	21.4	55
3	Vulture Genomes Reveal Molecular Adaptations Underlying Obligate Scavenging and Low Levels of Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2021, 38, 3649-3663.	8.9	9
4	High-quality genome assembly and resequencing of modern cotton cultivars provide resources for crop improvement. <i>Nature Genetics</i> , 2021, 53, 1385-1391.	21.4	76
5	Building a Chinese pan-genome of 486 individuals. <i>Communications Biology</i> , 2021, 4, 1016.	4.4	13
6	Association of female reproductive tract microbiota with egg production in layer chickens. <i>GigaScience</i> , 2021, 10, .	6.4	7
7	Genomic analyses reveal selection footprints in rice landraces grown under on-farm conservation conditions during a short-term period of domestication. <i>Evolutionary Applications</i> , 2020, 13, 290-302.	3.1	9
8	Genomic Analyses Reveal Genetic Adaptations to Tropical Climates in Chickens. <i>IScience</i> , 2020, 23, 101644.	4.1	28
9	A Chromosome-Level Genome Assembly of Garlic (<i>Allium sativum</i>) Provides Insights into Genome Evolution and Allicin Biosynthesis. <i>Molecular Plant</i> , 2020, 13, 1328-1339.	8.3	89
10	Molecular adaptation and convergent evolution of frugivory in Old World and neotropical fruit bats. <i>Molecular Ecology</i> , 2020, 29, 4366-4381.	3.9	32
11	Microevolutionary Dynamics of Chicken Genomes under Divergent Selection for Adiposity. <i>IScience</i> , 2020, 23, 101193.	4.1	9
12	Population genomics identifies patterns of genetic diversity and selection in chicken. <i>BMC Genomics</i> , 2019, 20, 263.	2.8	34
13	Large-scale inversions majorly drive upland cotton population differentiation. <i>Journal of Cotton Research</i> , 2019, 2, .	2.5	0
14	Genome re-sequencing reveals the evolutionary history of peach fruit edibility. <i>Nature Communications</i> , 2018, 9, 5404.	12.8	84
15	Genome-Wide Chromatin Structure Changes During Adipogenesis and Myogenesis. <i>International Journal of Biological Sciences</i> , 2018, 14, 1571-1585.	6.4	23
16	Population genomics of wild Chinese rhesus macaques reveals a dynamic demographic history and local adaptation, with implications for biomedical research. <i>GigaScience</i> , 2018, 7, .	6.4	27
17	Resequencing a core collection of upland cotton identifies genomic variation and loci influencing fiber quality and yield. <i>Nature Genetics</i> , 2018, 50, 803-813.	21.4	368
18	Genomic analyses of primitive, wild and cultivated citrus provide insights into asexual reproduction. <i>Nature Genetics</i> , 2017, 49, 765-772.	21.4	316

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19	Genomic data for 78 chickens from 14 populations. <i>GigaScience</i> , 2017, 6, 1-5.	6.4	28
20	Exosomal microRNAs in giant panda (<i>Ailuropoda melanoleuca</i>) breast milk: potential maternal regulators for the development of newborn cubs. <i>Scientific Reports</i> , 2017, 7, 3507.	3.3	86
21	Comprehensive variation discovery and recovery of missing sequence in the pig genome using multiple de novo assemblies. <i>Genome Research</i> , 2017, 27, 865-874.	5.5	116
22	Comparative transcriptomics of 5 high-altitude vertebrates and their low-altitude relatives. <i>GigaScience</i> , 2017, 6, 1-9.	6.4	50
23	mRNA N6-methyladenosine methylation of postnatal liver development in pig. <i>PLoS ONE</i> , 2017, 12, e0173421.	2.5	48
24	Genome-wide analysis reveals selection for Chinese Rongchang pigs. <i>Frontiers of Agricultural Science and Engineering</i> , 2017, 4, 319.	1.4	2
25	Comparative analysis of the microRNA transcriptome between yak and cattle provides insight into high-altitude adaptation. <i>PeerJ</i> , 2017, 5, e3959.	2.0	43
26	Detecting mitochondrial signatures of selection in wild Tibetan pigs and domesticated pigs. <i>Mitochondrial DNA</i> , 2016, 27, 747-752.	0.6	20
27	Transcriptomic analysis reveals distinct resistant response by physcion and chrysophanol against cucumber powdery mildew. <i>PeerJ</i> , 2016, 4, e1991.	2.0	24
28	Whole-Genome Sequencing of Native Sheep Provides Insights into Rapid Adaptations to Extreme Environments. <i>Molecular Biology and Evolution</i> , 2016, 33, 2576-2592.	8.9	271
29	A de novo silencer causes elimination of MITF-M expression and profound hearing loss in pigs. <i>BMC Biology</i> , 2016, 14, 52.	3.8	53
30	Reply to 'Olfactory genes in Tibetan wild boar (NG-CR42819)'. <i>Nature Genetics</i> , 2016, 48, 973-974.	21.4	0
31	Population Genomics Reveals Low Genetic Diversity and Adaptation to Hypoxia in Snub-Nosed Monkeys. <i>Molecular Biology and Evolution</i> , 2016, 33, 2670-2681.	8.9	69
32	Genomic analysis reveals selection in Chinese native black pig. <i>Scientific Reports</i> , 2016, 6, 36354.	3.3	32
33	Genomic Analyses Reveal Demographic History and Temperate Adaptation of the Newly Discovered Honey Bee Subspecies <i>Apis mellifera sinixinyuan</i> n. ssp. <i>Molecular Biology and Evolution</i> , 2016, 33, 1337-1348.	8.9	125
34	Detection of genetic diversity and selection at the coding region of the melanocortin receptor 1 (<i>MC1R</i>) in Tibetan wild boar (<i>Sus scrofa</i>). <i>PLoS ONE</i> , 2016, 11, e0160000.	2.2	8
35	Deciphering the microRNA transcriptome of skeletal muscle during porcine development. <i>PeerJ</i> , 2016, 4, e1504.	2.0	12
36	Dynamic gene expression profiles during postnatal development of porcine subcutaneous adipose. <i>PeerJ</i> , 2016, 4, e1768.	2.0	4

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37	Genetic responses to seasonal variation in altitudinal stress: whole-genome resequencing of great tit in eastern Himalayas. <i>Scientific Reports</i> , 2015, 5, 14256.	3.3	33
38	Whole Exome Sequencing Identifies Frequent Somatic Mutations in Cell-Cell Adhesion Genes in Chinese Patients with Lung Squamous Cell Carcinoma. <i>Scientific Reports</i> , 2015, 5, 14237.	3.3	51
39	Reply to 'Evolution of Tibetan wild boars'. <i>Nature Genetics</i> , 2015, 47, 189-190.	21.4	0
40	Reply to 'On genetic differentiation between domestic pigs and Tibetan wild boars'. <i>Nature Genetics</i> , 2015, 47, 192-192.	21.4	0
41	Transcriptomic analysis provides insight into high-altitude acclimation in domestic goats. <i>Gene</i> , 2015, 567, 208-216.	2.2	26
42	Whole-genome sequencing of Berkshire (European native pig) provides insights into its origin and domestication. <i>Scientific Reports</i> , 2015, 4, 4678.	3.3	81
43	Snapshot of Structural Variations in the Tibetan Wild Boar Genome at Single-Nucleotide Resolution. <i>Journal of Genetics and Genomics</i> , 2014, 41, 653-657.	3.9	6
44	Genomic analyses identify distinct patterns of selection in domesticated pigs and Tibetan wild boars. <i>Nature Genetics</i> , 2013, 45, 1431-1438.	21.4	472
45	Ground tit genome reveals avian adaptation to living at high altitudes in the Tibetan plateau. <i>Nature Communications</i> , 2013, 4, 2071.	12.8	229